



Figure S1. See legend over page

**Figure S1** Microprocessor Modulates the Splicing Efficiency and Expression Level of DICER. **(A)** Extracts of HeLa cells transfected with control or DROSHA-specific siRNA were analyzed by immunoblot using the antibodies indicated. **(B)** Extracts of 293T cells transfected with control or DGCR8-specific siRNA were analyzed by immunoblot using the antibodies indicated. **(C)** Extracts of 293T cells transfected with siRNA targeting AGO2, p54/Rck, XRN1, LSM1 or a non-targeting control were analyzed by immunoblot using the indicated antibodies. **(D)** Extracts of HeLa cells transfected with control or DROSHA-specific siRNA were analyzed by RT-qPCR using PCR primers specifically amplifying spliced or unspliced transcripts as indicated on the schematic above the graph. Values obtained for the control sample (siScr) were attributed a value of 1. Data are represented as mean  $\pm$  SEM ( $*P < 0.05$ , independent Student *t* test) **(E)** Extracts of control or DROSHA knock-down HeLa cells were analyzed by RT-qPCR using PCR primers specifically amplifying spliced or unspliced transcripts. The splicing efficiency was calculated by the ratio of spliced to unspliced transcripts. Values obtained for the control sample (siScr) were attributed a value of 1. Data represent mean  $\pm$  SEM obtained from 3 independent experiments ( $***P < 0.001$ , independent Student *t* test). **(F-H)** Drosha knock-down does not enhance splicing efficiency of all pre-mRNAs. Extracts of control or DROSHA knock-down 293T cells were analyzed by RT-qPCR using PCR primers specifically amplifying spliced or unspliced transcripts of CTDSPL, shown in **F**, CTDSP1, shown in **G**, and GAPDH, shown in **H**. The splicing efficiency was calculated by the ratio of spliced to unspliced transcripts. Values obtained for the control sample (siScr) were attributed a value of 1. Data represent mean  $\pm$  SEM obtained from 3 independent experiments ( $***P < 0.001$ , independent Student *t* test).